

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gregory, Richard J.
Wills, Ken N.
Maneval, Daniel C.

(ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
Methods of Use

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Campbell and Flores
(B) STREET: 4370 La Jolla Village Drive, Suite 700
(C) CITY: San Diego
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/328,673
(B) FILING DATE: 25-OCT-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/233,777
(B) FILING DATE: 19-MAY-1994

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/142,669
(B) FILING DATE: 25-OCT-1993

(ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: Campbell, Cathryn A.
(B) REGISTRATION NUMBER: 31,815
(C) REFERENCE/DOCKET NUMBER: P-CJ 1192

(x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (619) 535-9001
(B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCCACCGAG GGACCTGAGC GAGTC

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCTGGGAAG GGACAGAAGA

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGCTAGCT CTGCCCAAA GAGCT

25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGAAG

39

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGTGCAGCCG CTGGAGGACT TTGAGGATGT CTGTC

35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCTCTAGAG AGACCAAGTTA GGAAGTTTTC GCA

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 139..2922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTA CGGGAGTCGG GAGAGGACGG	60
GGCGTGCCTT GCGTGCAGGC GCGTCGTCTT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCCTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	171
1 5 10	
ACC GCC GCC GCT GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro	219
15 20 25	
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	267
30 35 40	
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	315
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	363
60 65 70 75	
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	411
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	459
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	507
110 115 120	

ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp 125 130 135	555
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr 140 145 150 155	603
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu 160 165 170	651
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser 175 180 185	699
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly 190 195 200	747
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met 205 210 215	795
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu 220 225 230 235	843
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg 240 245 250	891
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu 255 260 265	939
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys 270 275 280	987
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe 285 290 295	1035
ATG AAT TCT CTT GGA CTT GTC ACA TCT AAT GGA CTT CCA GAG GTT GAA Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu 300 305 310 315	1083
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu 320 325 330	1131
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser 335 340 345	1179
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp 350 355 360	1227
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met 365 370 375	1275
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln 380 385 390 395	1323

CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro 400 405 410	1371
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys 415 420 425	1419
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser 430 435 440	1467
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser 445 450 455	1515
ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys 460 465 470 475	1563
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu 480 485 490	1611
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp 495 500 505	1659
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu 510 515 520	1707
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu 525 530 535	1755
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His 540 545 550 555	1803
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp 560 565 570	1851
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu 575 580 585	1899
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala 590 595 600	1947
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr 605 610 615	1995
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala 620 625 630 635	2043
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr 640 645 650	2091
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu 655 660 665	2139

CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu 670 675 680	2187
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His 685 690 695	2235
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys 700 705 710 715	2283
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu 720 725 730	2331
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu 735 740 745	2379
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg 750 755 760	2427
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu 765 770 775	2475
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser 780 785 790 795	2523
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser 800 805 810	2571
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro 815 820 825	2619
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu 830 835 840	2667
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu 845 850 855	2715
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu 860 865 870 875	2763
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu 880 885 890	2811
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr 895 900 905	2859
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser 910 915 920	2907

67

AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT 2962
Asn Lys Glu Glu Lys
925

GGATTCATG TCTCTCACAG ATGTGACTGA TAT 2995

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1 5 10 15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
20 25 30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
35 40 45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50 55 60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65 70 75 80

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85 90 95

Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
100 105 110

Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
115 120 125

His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
130 135 140

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145 150 155 160

Leu Phe Ser Lys Leu Glu Arg Thr cys Glu Leu Ile Tyr Leu Thr Gln
165 170 175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
180 185 190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
195 200 205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
210 215 220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225 230 235 240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
245 250 255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
 260 265 270
 Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
 275 280 285
 Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
 290 295 300
 Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
 305 310 315 320
 Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
 325 330 335
 Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
 340 345 350
 Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
 355 360 365
 Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
 370 375 380
 Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
 385 390 395 400
 Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
 405 410 415
 Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
 420 425 430
 Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
 435 440 445
 Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
 450 455 460
 Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
 465 470 475 480
 Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
 485 490 495
 Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
 500 505 510
 Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
 515 520 525
 Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
 530 535 540
 Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
 545 550 555 560
 Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
 565 570 575
 Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
 580 585 590
 Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
 595 600 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
 610 615 620
 Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
 625 630 635 640
 Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
 645 650 655
 Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
 660 665 670
 His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
 675 680 685
 Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
 690 695 700
 Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
 705 710 715 720
 Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
 725 730 735
 Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
 740 745 750
 Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
 755 760 765
 Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
 770 775 780
 Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
 785 790 795 800
 Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
 805 810 815
 Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
 820 825 830
 Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
 835 840 845
 Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
 850 855 860
 Gly Ser Asn Pro Pro Lys Pro Leu Lys Leu Arg Phe Asp Ile Glu
 865 870 875 880
 Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
 885 890 895
 Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
 900 905 910
 Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 915 920 925

70

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa = stop codon"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "Xaa = stop codon"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 439
- (D) OTHER INFORMATION: /note= "Xaa = stop codon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val	Xaa	Ser	His	Arg	Pro	Gly	Ser	Arg	Xaa	Leu	Leu	Gly	Ser	Gly	Asp
1						5			10				15		

Thr	Leu	Arg	Ser	Gly	Trp	Glu	Arg	Ala	Phe	His	Asp	Gly	Asp	Thr	Leu
					20			25				30			

Pro	Trp	Ile	Gly	Ser	Gln	Thr	Ala	Phe	Arg	Val	Thr	Ala	Met	Glu	Glu
					35			40				45			

Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	Gln	Glu	Thr	Phe
					50			55			60				

Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu	Ser	Pro	Leu
					65			70			75			80	

Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu	Ser	Pro	Asp	Asp	Ile	Glu
					85			90				95			

Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro	Asp	Glu	Ala	Pro	Arg	Met	Pro
					100			105			110				

Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Ala	Pro	Thr	Pro	Ala		
					115			120			125				

Ala	Pro	Ala	Pro	Ala	Pro	Ser	Trp	Pro	Leu	Ser	Ser	Ser	Val	Pro	Ser
						130			135			140			

Gln	Lys	Thr	Tyr	Gln	Gly	Ser	Tyr	Gly	Phe	Arg	Leu	Gly	Phe	Leu	His
					145			150			155			160	

Ser	Gly	Thr	Ala	Lys	Ser	Val	Thr	Cys	Thr	Tyr	Ser	Pro	Ala	Leu	Asn
						165		170				175			

Lys	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr	Cys	Pro	Val	Gln	Leu	Trp	Val
						180			185			190			

Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	Arg	Ala	Met	Ala	Ile	Tyr
						195			200			205			

71

Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His
210 215 220

Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile
225 230 235 240

Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr
245 250 255

Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser
260 265 270

Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met
275 280 285

Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp
290 295 300

Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys
305 310 315 320

Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys
325 330 335

Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala
340 345 350

Leu Pro Asn Asn Thr Ser Ser Pro Gln Pro Lys Lys Lys Pro Leu
355 360 365

Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu
370 375 380

Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala
385 390 395 400

Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser
405 410 415

Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr
420 425 430

Glu Gly Pro Asp Ser Asp Xaa
435

TJ